

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/585,620
Source: IFWP
Date Processed by STIC: 7/21/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/585,620

CRF Edit Date: 7/21/06
Edited by: AZ

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

J Deleted: J invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

___ Other:



IFWP

RAW SEQUENCE LISTING

DATE: 07/21/2006

PATENT APPLICATION: US/10/585,620

TIME: 17:42:23

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\07212006\J585620.raw

3 <110> APPLICANT: Ye, Liu
 4 Lan, Tang
 5 Spendler, Tina
 7 <120> TITLE OF INVENTION: Amylase
 9 <130> FILE REFERENCE: 10583.204-US
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/585,620
 C--> 11 <141> CURRENT FILING DATE: 2006-07-08
 11 <160> NUMBER OF SEQ ID NOS: 17
 13 <170> SOFTWARE: PatentIn version 3.3
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 1946
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Chaetomium sp.
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (86)..(1843)
 25 <220> FEATURE:
 26 <221> NAME/KEY: sig_peptide
 27 <222> LOCATION: (86)..(145)
 29 <220> FEATURE:
 30 <221> NAME/KEY: mat_peptide
 31 <222> LOCATION: (146)..(1843)
 33 <400> SEQUENCE: 1
 34 tcccgggtcat cctctcttgg tccctgccat cctcctgccc cctctgatcc accgcctctt 60
 36 cggtggactc caagacgttg tcagg atg cga tcc ttc ctc gcc ctc tca gcc 112
 37 Met Arg Ser Phe Leu Ala Leu Ser Ala
 38 -20 -15
 40 ttg ctg ctg ctg tac ccg ctg cag ctg ctc gcc gcc agc aac tcc gac 160
 41 Leu Leu Leu Leu Tyr Pro Leu Gln Leu Leu Ala Ala Ser Asn Ser Asp
 42 -10 -5 -1 1 5
 44 tgg agg tcc cgc aat atc tac ttt gcc ttg acc gac cgc gtc gcc aat 208
 45 Trp Arg Ser Arg Asn Ile Tyr Phe Ala Leu Thr Asp Arg Val Ala Asn
 46 10 15 20
 48 ccg tcc acc acg acc gca tgt agt gac ctg agc aac tac tgc ggc ggc 256
 49 Pro Ser Thr Thr Thr Ala Cys Ser Asp Leu Ser Asn Tyr Cys Gly Gly
 50 25 30 35
 52 acg tgg agc ggc ctg tcg agc aag ctg gac tac atc caa ggg atg ggc 304
 53 Thr Trp Ser Gly Leu Ser Ser Lys Leu Asp Tyr Ile Gln Gly Met Gly
 54 40 45 50
 56 ttc gat tcc atc tgg att acc ccc gtg gtc gag aac tgc gac ggt ggc 352
 57 Phe Asp Ser Ile Trp Ile Thr Pro Val Val Glu Asn Cys Asp Gly Gly
 58 55 60 65
 60 tac cac ggc tac tgg gcc aag gcg ctc tac aac gtc aac acg aac tac 400

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61	Tyr	His	Gly	Tyr	Trp	Ala	Lys	Ala	Leu	Tyr	Asn	Val	Asn	Thr	Asn	Tyr	
62	70					75					80					85	
64	ggc	agt	gcg	gat	gat	ctg	aag	aac	ttc	gtt	gcg	gcc	gcc	cat	gcg	aag	448
65	Gly	Ser	Ala	Asp	Asp	Leu	Lys	Asn	Phe	Val	Ala	Ala	Ala	His	Ala	Lys	
66						90					95					100	
68	ggc	atg	tac	gtg	atg	gtg	gac	gtc	gtc	gcg	aat	cac	atg	ggt	tcc	tgc	496
69	Gly	Met	Tyr	Val	Met	Val	Asp	Val	Val	Ala	Asn	His	Met	Gly	Ser	Cys	
70						105					110					115	
72	ggc	atc	gcc	aac	ctc	tcc	cca	cct	ccc	ctg	aac	gag	cag	agc	tct	tat	544
73	Gly	Ile	Ala	Asn	Leu	Ser	Pro	Pro	Pro	Leu	Asn	Glu	Gln	Ser	Ser	Tyr	
74						120					125					130	
76	cac	acc	cag	tgc	gac	att	gac	tac	agc	agt	cag	tcc	agc	att	gag	acg	592
77	His	Thr	Gln	Cys	Asp	Ile	Asp	Tyr	Ser	Ser	Gln	Ser	Ser	Ile	Glu	Thr	
78						135					140					145	
80	tgc	tgg	ata	tcc	ggc	ctc	cct	gac	ctg	gac	acc	acc	gat	agc	act	atc	640
81	Cys	Trp	Ile	Ser	Gly	Leu	Pro	Asp	Leu	Asp	Thr	Thr	Asp	Ser	Thr	Ile	
82	150					155					160					165	
84	cga	tcc	ctc	ttc	cag	acc	tgg	gtc	cac	ggc	ctg	gtc	agc	aac	tac	agc	688
85	Arg	Ser	Leu	Phe	Gln	Thr	Trp	Val	His	Gly	Leu	Val	Ser	Asn	Tyr	Ser	
86						170					175					180	
88	ttc	gac	ggt	ctc	cgc	gtc	gac	acc	gtc	aag	cac	gtg	gag	aag	gat	tac	736
89	Phe	Asp	Gly	Leu	Arg	Val	Asp	Thr	Val	Lys	His	Val	Glu	Lys	Asp	Tyr	
90						185					190					195	
92	tgg	ccc	ggc	ttc	gtg	tcg	gcg	gcg	ggc	acc	tac	gcc	atc	ggc	gaa	gtc	784
93	Trp	Pro	Gly	Phe	Val	Ser	Ala	Ala	Gly	Thr	Tyr	Ala	Ile	Gly	Glu	Val	
94						200					205					210	
96	ttc	tcc	ggc	gac	acc	tcc	tac	gtg	gcc	ggc	tat	caa	tcg	gtg	atg	ccg	832
97	Phe	Ser	Gly	Asp	Thr	Ser	Tyr	Val	Ala	Gly	Tyr	Gln	Ser	Val	Met	Pro	
98						215					220					225	
100	ggc	ttg	ctc	aac	tat	ccc	atc	tac	tat	ccg	ctc	atc	cgc	gtc	ttc	gcg	880
101	Gly	Leu	Leu	Asn	Tyr	Pro	Ile	Tyr	Tyr	Pro	Leu	Ile	Arg	Val	Phe	Ala	
102	230					235					240					245	
104	cag	ggt	gcg	tcc	ttc	acc	gat	ctc	gtc	aac	aac	cac	gat	acc	gtc	ggc	928
105	Gln	Gly	Ala	Ser	Phe	Thr	Asp	Leu	Val	Asn	Asn	His	Asp	Thr	Val	Gly	
106						250					255					260	
108	tcg	acc	ttc	tcc	gac	ccg	acg	ctg	ctg	ggt	aac	ttt	atc	gac	aac	cac	976
109	Ser	Thr	Phe	Ser	Asp	Pro	Thr	Leu	Leu	Gly	Asn	Phe	Ile	Asp	Asn	His	
110						265					270					275	
112	gac	aac	cca	cgt	ttc	ctg	agc	tac	acc	agc	gac	cac	gcc	ctc	ctc	aag	1024
113	Asp	Asn	Pro	Arg	Phe	Leu	Ser	Tyr	Thr	Ser	Asp	His	Ala	Leu	Leu	Lys	
114						280					285					290	
116	aac	gct	ctg	gcc	tac	gtc	atc	ctg	gcc	aga	ggc	atc	ccc	atc	gtc	tac	1072
117	Asn	Ala	Leu	Ala	Tyr	Val	Ile	Leu	Ala	Arg	Gly	Ile	Pro	Ile	Val	Tyr	
118						295					300					305	
120	tac	ggc	acc	gag	caa	ggc	tac	tcg	ggt	tcg	tcc	gac	ccg	gcg	aac	cgc	1120
121	Tyr	Gly	Thr	Glu	Gln	Gly	Tyr	Ser	Gly	Ser	Ser	Asp	Pro	Ala	Asn	Arg	
122	310					315					320					325	
124	gag	gat	ctc	tgg	cgt	agc	gga	tac	agc	act	acg	gga	gac	atc	tac	acc	1168
125	Glu	Asp	Leu	Trp	Arg	Ser	Gly	Tyr	Ser	Thr	Thr	Gly	Asp	Ile	Tyr	Thr	

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Input Set : A:\PTO.AMC.txt

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126          330          335          340
128 acc atc gcc gcg ctc tcc gcc gcg cgc acc gcg gcc ggt ggc ctc gcc      1216
129 Thr Ile Ala Ala Leu Ser Ala Ala Arg Thr Ala Ala Gly Gly Leu Ala
130          345          350          355
132 ggt aac gac cac gtc cac ctg tac acg acc gac aac gcg tac gcc tgg      1264
133 Gly Asn Asp His Val His Leu Tyr Thr Thr Asp Asn Ala Tyr Ala Trp
134          360          365          370
136 tcc cgg gcg agc ggc aag ctc atc gtc gtc acg tcc aac cgc ggc agc      1312
137 Ser Arg Ala Ser Gly Lys Leu Ile Val Val Thr Ser Asn Arg Gly Ser
138          375          380          385
140 tcc gac agc agc acc atc tgc ttc agc acc cag cag gcc agc ggc acc      1360
141 Ser Asp Ser Ser Thr Ile Cys Phe Ser Thr Gln Gln Ala Ser Gly Thr
142 390          395          400          405
144 acc tgg acc agc acg atc acc ggc aac tcg tac acc gcc gac agc aac      1408
145 Thr Trp Thr Ser Thr Ile Thr Gly Asn Ser Tyr Thr Ala Asp Ser Asn
146          410          415          420
148 ggc cag atc tgc gtg cag ctg tcc agc ggc gga ccc gag gcg ctc gtc      1456
149 Gly Gln Ile Cys Val Gln Leu Ser Ser Gly Gly Pro Glu Ala Leu Val
150          425          430          435
152 gtc tcc acc gcg acc ggc acc gcc acc gcg acg act ctg tcc acg acc      1504
153 Val Ser Thr Ala Thr Gly Thr Ala Thr Ala Thr Thr Leu Ser Thr Thr
154          440          445          450
156 acc aag acg tcc acc tcg acc gcc tcc tgc gcc gcc acc gtc gcc gtc      1552
157 Thr Lys Thr Ser Thr Ser Thr Ala Ser Cys Ala Ala Thr Val Ala Val
158          455          460          465
160 acc ttc aac gag ctc gtc acc acg aac tac ggc gac acc atc cgc ctg      1600
161 Thr Phe Asn Glu Leu Val Thr Thr Asn Tyr Gly Asp Thr Ile Arg Leu
162 470          475          480          485
164 acg ggc tcc atc tcc cag ctc agc agc tgg agc gca acc tcc ggg ctg      1648
165 Thr Gly Ser Ile Ser Gln Leu Ser Ser Trp Ser Ala Thr Ser Gly Leu
166          490          495          500
168 gcc ctg agc gcg tcc gcg tac acg tcc agc aac ccg ctc tgg agc gtg      1696
169 Ala Leu Ser Ala Ser Ala Tyr Thr Ser Ser Asn Pro Leu Trp Ser Val
170          505          510          515
172 acg gtc agc ctg ccg gcc ggc acg tcg ttc gag tac aag ttc gtc cgc      1744
173 Thr Val Ser Leu Pro Ala Gly Thr Ser Phe Glu Tyr Lys Phe Val Arg
174          520          525          530
176 atc acg agc gac ggc acc gtg acc tgg gaa tcg gac ccg aac cgc agc      1792
177 Ile Thr Ser Asp Gly Thr Val Thr Trp Glu Ser Asp Pro Asn Arg Ser
178          535          540          545
180 tac acc gtc ccg acg tgc gcg agc acc gcg acg atc agc aat acc tgg      1840
181 Tyr Thr Val Pro Thr Cys Ala Ser Thr Ala Thr Ile Ser Asn Thr Trp
182 550          555          560          565
184 cgg tgagctctgg acgtgttgta catataggag gccgttgaga ggccggggcg      1893
185 Arg
188 gttggtggtc ggggtgaatg gggggttgat gctttttcgt tgtgtcggtg aga      1946
191 <210> SEQ ID NO: 2
192 <211> LENGTH: 586
193 <212> TYPE: PRT

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RAW SEQUENCE LISTING

DATE: 07/21/2006

PATENT APPLICATION: US/10/585,620

TIME: 17:42:23

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\07212006\J585620.raw

194 <213> ORGANISM: Chaetomium sp.

196 <400> SEQUENCE: 2

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198 Met Arg Ser Phe Leu Ala Leu Ser Ala Leu Leu Leu Tyr Pro Leu
199 -20 -15 -10 -5
202 Gln Leu Leu Ala Ala Ser Asn Ser Asp Trp Arg Ser Arg Asn Ile Tyr
203 -1 1 5 10
206 Phe Ala Leu Thr Asp Arg Val Ala Asn Pro Ser Thr Thr Ala Cys
207 15 20 25
210 Ser Asp Leu Ser Asn Tyr Cys Gly Gly Thr Trp Ser Gly Leu Ser Ser
211 30 35 40
214 Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Asp Ser Ile Trp Ile Thr
215 45 50 55 60
218 Pro Val Val Glu Asn Cys Asp Gly Gly Tyr His Gly Tyr Trp Ala Lys
219 65 70 75
222 Ala Leu Tyr Asn Val Asn Thr Asn Tyr Gly Ser Ala Asp Asp Leu Lys
223 80 85 90
226 Asn Phe Val Ala Ala Ala His Ala Lys Gly Met Tyr Val Met Val Asp
227 95 100 105
230 Val Val Ala Asn His Met Gly Ser Cys Gly Ile Ala Asn Leu Ser Pro
231 110 115 120
234 Pro Pro Leu Asn Glu Gln Ser Ser Tyr His Thr Gln Cys Asp Ile Asp
235 125 130 135 140
238 Tyr Ser Ser Gln Ser Ser Ile Glu Thr Cys Trp Ile Ser Gly Leu Pro
239 145 150 155
242 Asp Leu Asp Thr Thr Asp Ser Thr Ile Arg Ser Leu Phe Gln Thr Trp
243 160 165 170
246 Val His Gly Leu Val Ser Asn Tyr Ser Phe Asp Gly Leu Arg Val Asp
247 175 180 185
250 Thr Val Lys His Val Glu Lys Asp Tyr Trp Pro Gly Phe Val Ser Ala
251 190 195 200
254 Ala Gly Thr Tyr Ala Ile Gly Glu Val Phe Ser Gly Asp Thr Ser Tyr
255 205 210 215 220
258 Val Ala Gly Tyr Gln Ser Val Met Pro Gly Leu Leu Asn Tyr Pro Ile
259 225 230 235
262 Tyr Tyr Pro Leu Ile Arg Val Phe Ala Gln Gly Ala Ser Phe Thr Asp
263 240 245 250
266 Leu Val Asn Asn His Asp Thr Val Gly Ser Thr Phe Ser Asp Pro Thr
267 255 260 265
270 Leu Leu Gly Asn Phe Ile Asp Asn His Asp Asn Pro Arg Phe Leu Ser
271 270 275 280
274 Tyr Thr Ser Asp His Ala Leu Leu Lys Asn Ala Leu Ala Tyr Val Ile
275 285 290 295 300
278 Leu Ala Arg Gly Ile Pro Ile Val Tyr Tyr Gly Thr Glu Gln Gly Tyr
279 305 310 315
282 Ser Gly Ser Ser Asp Pro Ala Asn Arg Glu Asp Leu Trp Arg Ser Gly
283 320 325 330
286 Tyr Ser Thr Thr Gly Asp Ile Tyr Thr Thr Ile Ala Ala Leu Ser Ala
287 335 340 345
290 Ala Arg Thr Ala Ala Gly Gly Leu Ala Gly Asn Asp His Val His Leu

```

RAW SEQUENCE LISTING

DATE: 07/21/2006

PATENT APPLICATION: US/10/585,620

TIME: 17:42:23

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\07212006\J585620.raw

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291      350      355      360
294 Tyr Thr Thr Asp Asn Ala Tyr Ala Trp Ser Arg Ala Ser Gly Lys Leu
295 365      370      375      380
298 Ile Val Val Thr Ser Asn Arg Gly Ser Ser Asp Ser Ser Thr Ile Cys
299      385      390      395
302 Phe Ser Thr Gln Ala Ser Gly Thr Thr Trp Thr Ser Thr Ile Thr
303      400      405      410
306 Gly Asn Ser Tyr Thr Ala Asp Ser Asn Gly Gln Ile Cys Val Gln Leu
307      415      420      425
310 Ser Ser Gly Gly Pro Glu Ala Leu Val Val Ser Thr Ala Thr Gly Thr
311      430      435      440
314 Ala Thr Ala Thr Thr Leu Ser Thr Thr Thr Lys Thr Ser Thr Ser Thr
315 445      450      455      460
318 Ala Ser Cys Ala Ala Thr Val Ala Val Thr Phe Asn Glu Leu Val Thr
319      465      470      475
322 Thr Asn Tyr Gly Asp Thr Ile Arg Leu Thr Gly Ser Ile Ser Gln Leu
323      480      485      490
326 Ser Ser Trp Ser Ala Thr Ser Gly Leu Ala Leu Ser Ala Ser Ala Tyr
327      495      500      505
330 Thr Ser Ser Asn Pro Leu Trp Ser Val Thr Val Ser Leu Pro Ala Gly
331      510      515      520
334 Thr Ser Phe Glu Tyr Lys Phe Val Arg Ile Thr Ser Asp Gly Thr Val
335 525      530      535      540
338 Thr Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Thr Cys Ala
339      545      550      555
342 Ser Thr Ala Thr Ile Ser Asn Thr Trp Arg
343      560      565

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346 <210> SEQ ID NO: 3

347 <211> LENGTH: 18

348 <212> TYPE: DNA

349 <213> ORGANISM: Artificial

351 <220> FEATURE:

352 <223> OTHER INFORMATION: Primer amyD1

355 <220> FEATURE:

356 <221> NAME/KEY: misc_feature

357 <222> LOCATION: (3)..(3)

358 <223> OTHER INFORMATION: n is a, c, g, or t

360 <220> FEATURE:

361 <221> NAME/KEY: misc_feature

362 <222> LOCATION: (12)..(12)

363 <223> OTHER INFORMATION: n is a, c, g, or t

365 <400> SEQUENCE: 3

W--> 366 gntaccayg gntactgg

18

369 <210> SEQ ID NO: 4

370 <211> LENGTH: 17

371 <212> TYPE: DNA

372 <213> ORGANISM: Artificial

374 <220> FEATURE:

375 <223> OTHER INFORMATION: Primer amyD2R

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/585,620

DATE: 07/21/2006
TIME: 17:42:24

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\07212006\J585620.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 3,12
Seq#:4; N Pos. 15
Seq#:5; N Pos. 15
Seq#:6; N Pos. 3,6,15
Seq#:7; N Pos. 3,6,15
Seq#:8; N Pos. 3,6,15
Seq#:13; Xaa Pos. 9

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,14,15,16,17

VERIFICATION SUMMARY

DATE: 07/21/2006

PATENT APPLICATION: US/10/585,620

TIME: 17:42:24

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\07212006\J585620.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0

**Raw Sequence Listing before editing
(for reference only)**



IFWP

RAW SEQUENCE LISTING

DATE: 07/19/2006

PATENT APPLICATION: US/10/585,620

TIME: 08:29:59

Input Set : A:\01-SQ Listing-06 Jul 2006.txt

Output Set: N:\CRF4\07192006\J585620.raw

3 <110> APPLICANT: Ye, Liu
4 Lan, Tang
5 Spendler, Tina
7 <120> TITLE OF INVENTION: Amylase
9 <130> FILE REFERENCE: 10583.204-US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/585,620
C--> 11 <141> CURRENT FILING DATE: 2006-07-08
11 <160> NUMBER OF SEQ ID NOS: 17
13 <170> SOFTWARE: PatentIn version 3.3

**Does Not Comply
Corrected Diskette Needed**

ERRORED SEQUENCES

594 <210> SEQ ID NO: 17
595 <211> LENGTH: 29
596 <212> TYPE: DNA
597 <213> ORGANISM: Artificial
599 <220> FEATURE:
600 <223> OTHER INFORMATION: Primer AM835.2
602 <400> SEQUENCE: 17
603 cgtctcgagg acacaacgaa aaagcatca
E--> 609 11

29

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/19/2006
PATENT APPLICATION: US/10/585,620 TIME: 08:30:00

Input Set : A:\01-SQ Listing-06 Jul 2006.txt
Output Set: N:\CRF4\07192006\J585620.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,14,15,16,17

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/585,620

DATE: 07/19/2006

TIME: 08:30:00

Input Set : A:\01-SQ Listing-06 Jul 2006.txt

Output Set: N:\CRF4\07192006\J585620.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
 L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
 L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
 L:402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
 L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
 L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
 L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
 L:550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
 L:609 M:254 E: No. of Bases conflict, this line has no nucleotides.